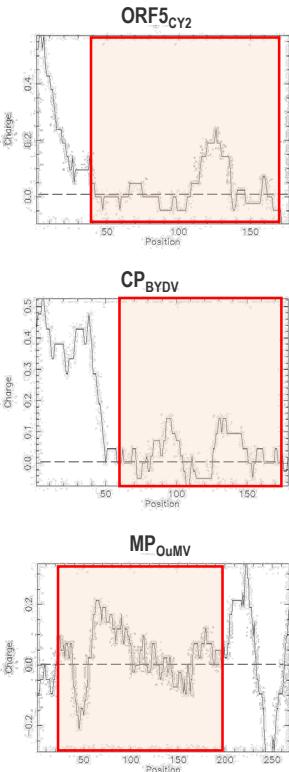


A

OuMV 30K MP	L - A R G Q I A V V D T R V - - -
SeMV CP	T - - A G S I H M G F Q Y D M - A
PULV	T - - Q - - I V G I G N A P S K D
JgULV	T - - Q - - I V G L G N C H S S V
TULV	T - - Q - - I V G L A N A D G - A
MULV	T - - Q - - I V G L A N A D G - A
EMaV	T - - Q - - I A G V G N A D S F Q
SULV	T - - Q - - I C G V G N A D Y Y T
EMaV	T - - Q - - I A G V G N A D S Y Q
FULV	T - - Q - - H C G V G L S S S G A
CY2	T - - Q - - L C G V G L S T S G A
OULV	T - - Q - - H C G V G L A T S G A
PEMV2 30K MP	V L G E V E I W L H D S I L P H L
CMoV 30K MP	S P G Q A V I W V H D T A L P G L
TMV 30K MP	C R G G V S V C L V D K R M E R A
Consensus	e e e e e

B

S7 Fig. ORF5 proteins have features inconsistent with canonical 30K MPs. **A.** Alignment of ORF5 proteins with selected 30K MPs. Critical 30K MP aspartic acid residue (D) is in red. Bottom row denotes the consensus secondary structure predicted in PROMALS3D where e represents a β -strand. **B.** Charge distribution for ORF5_{CY2}, CP_{BYDV}, and MP_{OuLV} by amino acid residue position (window size = 5) analyzed in EMBOSS CHARGE version 6.6.0. Red box denotes the jelly-roll domain. Note that charged residues are concentrated in the N-terminal region of ORF5_{CY2} and CP_{BYDV} but not MP_{OuLV}.